



# STIC Search Report

## Biotech-Chem Library

STIC Database Tracking Number: 151906

TO: Vanessa L Ford  
Location: rem/3b25/3c18  
Art Unit: 1645  
Friday, April 29, 2005

Case Serial Number: 10/017168

From: Toby Port

Location: Biotech-Chem Library  
REM1-A59

Phone: 272-2523

[toby.port@uspto.gov](mailto:toby.port@uspto.gov)

### Search Notes

Dear Examiner Ford,

Here are the results of your search.

Please feel free to contact me if you have any questions.

Toby Port

STIC-Biotech/ChemLib

151906

mg

From: Chan, Christina  
Sent: Wednesday, April 27, 2005 5:10 PM  
To: Ford, Vanessa; STIC-Biotech/ChemLib  
Subject: RE: In re: 10/017, 168 Sequence search

Please rush. Thanks Chris

Chris Chan

TC 1600 New Hire Training Coordinator and SPE 1644  
(571)-272-0841  
Remsen, 3E89

RECEIVED  
APR 28 2005  
STIC-Biotech/ChemLib  
(STIC)

-----Original Message-----

From: Ford, Vanessa  
Sent: Wednesday, April 27, 2005 3:11 PM  
To: Chan, Christina  
Subject: In re: 10/017, 168 Sequence search

Please search SEQ ID NOs: 7, 8, 10, 22, 24 and 26. Please include interference searches. Please rush.

Vanessa L. Ford  
Biotechnology Patent Examiner  
Office: REM 3B25  
Mailbox: REM 3C18  
Phone: 571.272.0857  
Art unit: 1645

\*\*\*\*\*

STAFF USE ONLY

Searcher: \_\_\_\_\_  
Searcher Phone: 2- \_\_\_\_\_  
Date Searcher Picked up: \_\_\_\_\_  
Date Completed: \_\_\_\_\_  
Searcher Prep/Rev. Time: \_\_\_\_\_  
Online Time: \_\_\_\_\_

\*\*\*\*\*

Type of Search

NA#: \_\_\_\_\_ AA#: \_\_\_\_\_  
Interference: \_\_\_\_\_ SPDI: \_\_\_\_\_  
S/L: \_\_\_\_\_ Oligomer: \_\_\_\_\_  
Encode/Transl: \_\_\_\_\_  
Structure#: \_\_\_\_\_ Text: \_\_\_\_\_  
Inventor: \_\_\_\_\_ Litigation: \_\_\_\_\_

\*\*\*\*\*

Vendors and cost where applicable

STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
QUESTEL/ORBIT: \_\_\_\_\_  
LEXIS/NEXIS: \_\_\_\_\_  
SEQUENCE SYSTEM: \_\_\_\_\_  
WWW/Internet: \_\_\_\_\_  
Other(Specify): \_\_\_\_\_

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: April 28, 2005, 16:36:51 ; Search time 91.7784 Seconds  
(without alignments)  
2192.749 Million cell updates/sec

Title: US-10-017-168-26

Perfect score: 2005  
Sequence: 1 MFVRSMDMPKNTAVESINLE.....AVLENFGFGKDAFLKKAR 393

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: UniProt 03:\*

1: uniprot\_sprot:\*

2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2005	100.0	393	093CA3	093CA3 treponema p
2	1977.5	98.6	428	09ALV6	09ALV6 treponema p
3	1899.5	94.7	548	093CA4	093CA4 treponema p
4	1743.5	87.0	348	09ALV7	09ALV7 treponema p
5	1286.5	64.2	432	051953	051953 treponema p
6	1043.5	52.0	227	083449	083449 treponema p
7	950.5	47.4	256	083448	083448 treponema p
8	504.5	25.2	458	073MG7	073MG7 treponema d
9	212.5	10.6	394	0964D0	0964D0 encephalito
10	212.5	10.6	453	1 PTP1 ENCHE	076273 encephalito
11	211	10.5	432	0964C9	0964C9 encephalito
12	210.5	10.5	410	096214	096214 encephalito
13	205	10.2	1112	063596	063596 bacillus ce
14	189	9.4	1167	07SH94	07SH94 neocospira
15	184	9.2	407	1 IE68 SHV21	001042 salmelline
16	184	9.2	1070	081YTO	081YTO bacillus an
17	182.5	9.1	630	1 YCF2 OENVI	031569 cenothea v
18	181.5	9.1	614	2 YCF2 OENVI	094674 plasmodium
19	180.5	9.0	466	2 OENVI	094674 plasmodium
20	180	9.0	5458	2 O9U459	09U459 plasmodium
21	179	8.9	3455	2 O6R5A9	06R5A9 tenebrio mo
22	176	8.8	687	2 O7S7J3	07S7J3 neocospira
23	175	8.7	675	2 O871R0	0871R0 neocospira
24	174	8.7	1271	2 O2S860	02S860 plasmodium
25	172	8.6	690	2 O6PCS2	06PCS2 plasmodium
26	170.5	8.5	601	2 O711E3	0711E3 streptococc
27	170.5	8.5	2768	2 O9VC00	09VC00 dirosophila
28	170	8.5	1233	2 O81U56	081U56 plasmodium
29	169.5	8.5	1554	2 O7RXX1	07RXX1 plasmodium
30	169	8.4	721	1 YCF2 OENVI	031568 cenothea p
31	169	8.4	697	2 O13058	013058 xenopus lae

32	168.5	8.4	1108	2 Q9ND10	Q9ND10 babeisia big
33	167.5	8.4	716	2 Q801T3	Q801T3 xenopus lae
34	167.5	8.4	843	2 Q6G1M0	Q6G1M0 xenopus lae
35	167.5	8.4	10578	2 O81SF5	O81SF5 caenorhabdi
36	167.5	8.4	18519	2 O81SF6	O81SF6 caenorhabdi
37	167.5	8.4	18534	2 O81SF7	O81SF7 caenorhabdi
38	166	8.3	544	1 INVO AOTTR	P24708 raphanus sa
39	164	8.2	248	2 Q9LRH2	Q9LRH2 raphanus sa
40	164	8.2	1236	2 Q9GTX2	Q9GTX2 plasmodium
41	162.5	8.1	1110	2 Q91255	Q91255 petromyzon
42	162	8.1	519	2 Q7S118	Q7S118 neocospira
43	162	8.1	722	2 Q26893	Q26893 trypanosoma
44	162	8.1	1142	2 Q8T6B4	Q8T6B4 dictyosteli
45	161	8.0	1964	2 Q59947	Q59947 streptococc

## ALIGNMENTS

RESULT 1  
093CA3 PRELIMINARY; PRT; 393 AA.  
AC 093CA3;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
DE Acidic repeat protein.  
GN Name=arp; pallidum (subsp. perenne) (Yaws treponema).  
OS Treponema pallidum (subsp. perenne) (Yaws treponema).  
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.  
OX NCBI\_TaxID=168;  
RN (1)  
RC SEQUENCE FROM N.A.  
RP STRAIN=CDCL;  
RA Liu H., Steiner B.M., Rodas B.;  
RL Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF411126; AAL07373.1;  
SQ SEQUENCE 393 AA; 42852 MW; C2D9198AA1B82B5 CRC64;

Query Match 100.0%; Score 2005; DB 2; Length 393;  
Best local similarity 100.0%; Pred. No. 1.8e-104;  
Matches 393; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MFVRSMDMPKNTAVESINLEKNAQAQAVVIGAGIGLLVSLAPAAAQGLGIVYQAVRV	60
DB	1	MFVRSMDMPKNTAVESINLEKNAQAQAVVIGAGIGLLVSLAPAAAQGLGIVYQAVRV	60
QY	61	RVRTLTGTVRGSGQTSQDGLSLASLPSRVPARPAQDPSSPPAGHTVPEYRDTVI	120
DB	61	RVRTLTGTVRGSGQTSQDGLSLASLPSRVPARPAQDPSSPPAGHTVPEYRDTVI	120
QY	121	LVSPLSRGGEREVDVKKVVPASERGEREVDVKKVVPASERGEREVDVKKV	180
DB	121	LVSPLSRGGEREVDVKKVVPASERGEREVDVKKVVPASERGEREVDVKKV	180
QY	181	VEPASERGEREVDVKKVVPASERGEREVDVKKVVPASERGEREVDVKKV	240
DB	181	VEPASERGEREVDVKKVVPASERGEREVDVKKVVPASERGEREVDVKKV	240
QY	241	VEPASERGEREVDVKKVVPASERGEREVDVKKVVPASERGEREVDVKKV	300
DB	241	VEPASERGEREVDVKKVVPASERGEREVDVKKVVPASERGEREVDVKKV	300
QY	301	GRAHPQVLPKAPGLQGEYVQIAVPHDAIOVOSTVHRGVYPTAVEDDIEGKRF	360
DB	301	GRAHPQVLPKAPGLQGEYVQIAVPHDAIOVOSTVHRGVYPTAVEDDIEGKRF	360
QY	361	TVVGVGVQKDERGAVLENFGFGKDAFLKKAR	393
DB	361	TVVGVGVQKDERGAVLENFGFGKDAFLKKAR	393

RESULT 2



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OM protein - protein search, using sw model

Run on: April 28, 2005, 16:35:11 ; Search time 98.5021 Seconds

(without alignments)  
1543.082 Million cell updates/sec

Title: US-10-017-168-26

Perfect score: 1 MFVRSDMFPRKNTAVEISNLE.....AVLENFQRFKDAFLKKAR 393

Sequence:

Scoring table: BLOSUM62

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :  
1: Geneseq\_16Dec04:\*  
2: geneseqp1980s:\*  
3: geneseqp1990s:\*  
4: geneseqp2000s:\*  
5: geneseqp2001s:\*  
6: geneseqp2002s:\*  
7: geneseqp2003as:\*  
8: geneseqp2003bs:\*  
9: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1364.5	68.1	312	4 AAB48318	Aab48318 T. pallid
2	1286.5	64.2	432	4 AAB48316	Aab48316 T. pallid
3	1130.5	56.4	232	4 AAB48317	Aab48317 T. pallid
4	187.5	9.4	1018	2 AAR98747	Aar98747 P. vivax
5	187.5	9.4	1018	2 AAW97039	Aaw97039 A. secreta
6	187.5	9.4	1018	2 AAG65528	Aag65528 Plasmodiu
7	187.5	9.4	1018	8 ADJ95471	Adj95471 Plasmodiu
8	182	9.1	783	2 AAR05804	Aar05804 C-termina
9	170.5	8.5	2768	4 ABB68397	Abb68397 Drosophila
10	167.5	8.4	2109	8 ADN23693	Adn23693 Bacterial
11	163	8.1	552	7 ADC31182	Adc31182 Human nov
12	162.5	8.1	1965	8 ADK47314	Adk47314 Streptococ
13	162.5	8.1	1972	6 ADK47314	Adk47314 Streptococ
14	160.5	8.0	1963	6 ABU46054	Abu46054 Protein e
15	157	7.8	1965	2 AAW69165	Aaw69165 Streptococ
16	156	7.8	278	2 AAW55109	Aaw55109 Streptococ
17	156	7.8	278	5 ABP54603	Abp54603 S. pneumo
18	156	7.8	278	7 ADC45175	Adc45175 S. pneumo
19	156	7.8	571	2 AAW55064	Aaw55064 Streptococ
20	156	7.8	571	5 ABP54558	Abp54558 S. pneumo
21	156	7.8	2004	7 ADC45085	Adc45085 S. pneumo
22	156	7.8	2004	8 ABU01577	Abu01577 S. pneumo
23	156	7.8	2004	8 ADM92167	Adm92167 S. pneumo
24	155	7.7	1000	6 ABJ25647	Abj25647 Aepexg111
25	154	7.7	795	4 ABB61567	Abb61567 Drosophila

26	152.5	7.6	486	5 AAE23036	Aae23036 Human thi
27	152	7.6	428	6 ABU44065	Abu44065 Protein e
28	151.5	7.6	2468	6 ABR64281	AbR64281 Angiogene
29	151.5	7.6	2468	7 ADE62723	Ade62723 Human Pro
30	151.5	7.6	2468	7 ADE62719	Ade62719 Human Pro
31	151.5	7.6	2468	7 ADE62727	Ade62727 Human Pro
32	151.5	7.6	2468	7 ADE62715	Ade62715 Human Pro
33	151.5	7.6	2468	8 ADL12997	Adl12997 Human ste
34	151.5	7.6	2468	8 ADN05260	Adn05260 Antipeori
35	151.5	7.6	2468	8 ADRI4614	Adri4614 Human NF-
36	151.5	7.6	2519	4 ABG16636	Abg16636 Novel hum
37	151.5	7.6	2527	8 ADN04561	Adn04561 Antipeori
38	150	7.5	522	4 AAE02397	Aae02397 Canine re
39	150	7.5	925	8 ADM97706	Adm97706 Murine NM
40	148.5	7.4	591	5 ABB92325	Abb92325 Herbicida
41	148.5	7.4	34350	8 AD089964	Ad089964 Antagonis
42	147.5	7.4	788	4 ABB68264	Abb68264 Drosophila
43	147	7.3	669	4 AAO12939	Aao12939 Human pol
44	147	7.3	905	2 AAW31186	Aaw31186 Human p16
45	147	7.3	983	8 ADM87342	Adm87342 Human pro

#### ALIGNMENTS

RESULT 1  
AAB48318  
ID AAB48318 standard; protein; 312 AA.

AC AAB48318;  
XX  
DT 11-SEP-2003 (revised)  
DT 20-APR-2001 (first entry)  
XX  
DE T. pallidum ssp. endemicum (Bosnia) acidic repeat protein (arp).  
XX  
KM Treponema pallidum; acidic repeat protein; arp; immunogenic; syphilis;  
XX  
KW yaws; bejel.

OS Treponema pallidum; ssp. endemicum.  
XX  
PN W0200077486-A2.

PD 21-DEC-2000.  
XX  
PF 14-JUN-2000; 2000WO-US016425.  
XX  
PR 14-JUN-1999; 99US-0138981P.

PI (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
XX  
PI Liu H, Steiner B, Rhodes B;

DR WPI: 2001-080711/09.  
XX  
DR N-PSDB; AAC84649.

PT Detecting Treponema pallidum in blood, saliva, etc., by detecting  
PT formation of a complex between immunogenic peptides of acidic repeat  
PT protein of the bacterium and an antibody present in the biological  
PT sample.

PS Claim 15; Fig 10; 73pp; English.

XX The invention relates to a method of detecting presence of Treponema  
XX pallidum (TP), anti-treponemal antibodies (Abs), or both in a biological  
XX sample that involves contacting an acidic repeat protein (arp), or one or  
XX more isolated immunogenic TP peptides of arp with an Ab containing  
XX biological sample and then detecting the formation of a complex between  
XX immunogenic peptides and Ab. The presence of the complex indicates the  
XX presence of TP. The method is thus useful for diagnosing syphilis, yaws,  
XX and bejel diseases. The immunogenic peptides or the Abs raised against  
XX arp, as part of an immunogenic composition, are useful for inducing a  
XX protective immune response against syphilis, yaws or bejel caused by TP.

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OM protein - protein search, using sw model

Run on: April 28, 2005, 16:51:57 ; Search time 23.0659 seconds  
(without alignments)  
1785.355 Million cell updates/sec

Title: US-10-017-168-24

Perfect score: 2180  
Sequence: 1 MEVRSDMPKNTAVEISNLE.....AVLENQRFGRDAFLKKAR 428

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	1043.5	47.9	227 2	G71326 hypothetical prote
2	963	44.2	256 2	F71326 hypothetical prote
3	212.5	9.7	407 1	EDBE03 immediate-early pr
4	206.5	9.5	1271 2	A45555 glutamate rich pr
5	203	9.3	721 2	S29795 hypothetical prote
6	197.5	9.1	2109 2	E89066 protein H05009.1 f
7	197.5	9.1	2109 2	T33247 NF-180 - sea lampre
8	190.5	8.7	1110 2	I51116 hypothetical prote
9	190	8.7	630 2	S29796 involucrin L - dou
10	188	8.6	544 1	I36911 neurofilament prot
11	183.5	8.4	913 2	T52485 ubiquitinol-cytochro
12	180	8.3	450 1	C29413 surface antigen Tc
13	178	8.2	391 2	S27850 elastic titin - hu
14	177	8.1	7962 2	I38346 protein kinase - s
15	176.5	8.1	1094 2	S49313 hypothetical prote
16	172	7.9	1252 2	T22523 hypothetical prote
17	170.5	7.8	1621 2	A82255 glutamic acid-rich
18	169	7.8	550 2	A40437 IGA-specific metal
19	166	7.6	1963 2	B98002 I2 protein - Trypa
20	165.5	7.6	506 2	S47436 flagellar antigen
21	165	7.6	411 2	S47436 hypothetical prote
22	164.5	7.5	5170 2	S28366 recombinaton repa
23	164	7.5	679 2	AC2807 Ompa family protei
24	163	7.5	754 2	B97867 hypothetical prote
25	163	7.5	754 2	B97867 hypothetical prote
26	163	7.4	1076 1	QFHHH neurofilament trip
27	161	7.3	296 2	AS4527 110k antigen - pla
28	159.5	7.3	2004 2	F95133 immunoglobulin A1
29	159.5	7.3	2004 2	F95133

30	159	7.3	1881 2	H95076 zinc metalloprotei
31	158.5	7.3	837 2	JN0292 antigen 332 - ma
32	158.5	7.3	845 2	A45659 neurofilament trip
33	158.5	7.3	1566 2	A43607 cell surface antig
34	158	7.2	518 2	G84488 En/Spm-like transp
35	157	7.2	298 1	I36912 involucrin S - dou
36	156	7.2	849 2	S00030 neurofilament trip
37	154.5	7.1	1876 2	E97944 zinc metalloprotei
38	152.5	7.0	1560 2	T30282 calcium-binding pr
39	151.5	6.9	333 2	T10738 hypothetical prote
40	150.5	6.9	798 2	T33022 hypothetical prote
41	150.5	6.9	1087 2	T30330 gelsolin-related p
42	150	6.9	419 2	G75062 probable flagella-
43	149.5	6.9	837 2	T02761 outer arm dynein i
44	149	6.8	592 1	LLBY actin-binding prot
45	149	6.8	798 2	150479 neurofilament medi

#### ALIGNMENTS

RESULT 1  
G71326  
hypothetical protein TP0434 - syphilis spirochete  
C:Species: Treponema pallidum subsp. pallidum (syphilis spirochete)  
C:Date: 24-Jul-1998 #sequence\_revision 24-Jul-1998 #text\_change 09-Jul-2004  
C:Accession: G71326  
R:Fraser, C.M.; Norris, S.J.; Weinstein, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwrt  
rson, J.; Knaluk, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Uetereback, T.; McDc  
they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.  
Science 281, 375-388, 1998  
A:Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.  
A:Reference number: A71250; MUID:98332770; PMID:9665876  
A:Accession: G71326  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-227 <COU>  
A:Cross-references: UNIPROT:O83449; GB:AE001220; GB:AE000520; NID:g3322705; PIDN:AAC654;  
A:Experimental source: strain Nichols  
A:Genetics:  
A:Gene: TP0434

Query Match 47.9%; Score 1043.5; DB 2; Length 227;  
Best Local Similarity 91.2%; Pred. No. 1.3e-54;  
Matches 207; Conservative 2; Mismatches 17; Indels 1; Gaps 1;

QY	202	REGGERVEDVPKVEPASEREGGERVEDVPKVEPASEREGGERVEDVPKVEPASE	261
DB	2	REGSVR-WTRCRRYVEPASEREGGEREGCGIPKVEPASEREGGERVEDVPKVEPASEG	60
QY	262	REGGERVEDVPKVEPASEREGGERVEDVPKVEPASEREGGERVEDVPKVEPASE	321
DB	61	HEGGERVEDVPKVEPASEREGGERVEDVPKVEPASEREGGERVEDVPKVEPASE	120
QY	322	DLSESEIVPEEOKGRAPQVITPEGAPRGLOPGEYVQIAVFNDAICVQSIIVHVGVEYP	381
DB	121	DLSESEIVPEEOKGRAPQVITPEGAPRGLOPGEYVQIAVFNDAICVQSIIVHVGVEYP	180
QY	382	IIVEDODIHGKVRFTVCYGPVQKDERGAVLENFORPFGKDAFLKKAR	428
DB	181	IIVEDODIHGKVRFTVCYGPVQKDERGAVLENFORPFGKDAFLKKAR	227

RESULT 2  
F71326  
hypothetical protein TP0433 - syphilis spirochete  
C:Species: Treponema pallidum subsp. pallidum (syphilis spirochete)  
C:Date: 24-Jul-1998 #sequence\_revision 24-Jul-1998 #text\_change 09-Jul-2004  
C:Accession: F71326  
R:Fraser, C.M.; Norris, S.J.; Weinstein, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwrt  
rson, J.; Knaluk, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Uetereback, T.; McDc  
they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.  
Science 281, 375-388, 1998

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# OM protein - protein search, using sw model

Run on: April 28, 2005, 16:35:11 ; Search time 107.275 Seconds  
(without alignments)  
1543.082 Million cell updates/sec

Title: US-10-017-168-24

Sequence: 1 MFVRSDFPKNATVEISNLE.....AVLENFQFGKDAFLKKAR 428

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database: A\_Geneseq\_16Dec04:\*  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No	Score	Query Match	Length DB	ID	Description
1	1567	71.9	312	4	AAB48318
2	1475	67.7	432	4	AAB48316
3	1113	51.1	232	4	AAB48317
4	214.5	9.8	1018	2	AAB98747
5	214.5	9.8	1018	2	AAW97039
6	214.5	9.8	1018	2	AAW97039
7	214.5	9.8	1018	2	AAW97039
8	204.5	9.4	783	2	AAW95471
9	201	9.2	2768	2	AAW95471
10	197.5	9.1	2109	8	ADN23653
11	192	8.8	552	7	ADN23653
12	183	8.4	1000	6	ADN23653
13	178	8.2	486	6	ADN23653
14	178	8.2	2468	6	ABR64281
15	178	8.2	2468	7	ABR64281
16	178	8.2	2468	7	ABR64281
17	178	8.2	2468	7	ABR64281
18	178	8.2	2468	7	ABR64281
19	178	8.2	2468	7	ABR64281
20	178	8.2	2468	8	ADN12997
21	178	8.2	2468	8	ADN12997
22	178	8.2	2468	8	ADN12997
23	178	8.2	2468	8	ADN12997
24	177	8.1	553	7	ADN04561
25	177	8.1	34350	8	ADN04561

26	171	7.8	194	4	ABG11265	Abg11265 Novel hum
27	171	7.8	522	4	AAE02397	Aae02397 Canine re
28	166	7.6	1963	6	ABU46054	Abu46054 Protein e
29	166	7.6	1965	8	ADK47314	Adk47314 Streptoco
30	166	7.6	1972	8	ADR44616	Adr44616 Novel S.
31	165.5	7.6	428	6	ABU44065	Abu44065 Protein e
32	164.5	7.5	795	4	ABE1567	Abt1567 Drosophila
33	164	7.5	669	4	AAO12939	Aac12939 Human pol
34	164	7.5	679	4	ABE59691	Abt59691 Drosophila
35	163	7.5	489	4	ABE58655	Abt58655 Drosophila
36	162.5	7.5	615	8	ADO19437	Adt19437 Human sof
37	162.5	7.5	615	8	ABM80918	Abm80918 Tumour-a8
38	162.5	7.5	1965	2	AAW69165	AAW69165 Streptoco
39	162	7.4	412	2	AAW03626	AAW03626 Human thy
40	161.5	7.4	864	4	AAW39026	AAW39026 Human pro
41	161.5	7.4	1026	4	AAW78825	AAW78825 Human hea
42	161.5	7.4	1388	7	ADJ69333	Adj69333 Human hea
43	161	7.4	617	4	AAW16458	AAW16458 Peptide #
44	161	7.4	617	4	ABE35445	Abt35445 Peptide #
45	161	7.4	617	4	ABB20884	Abb20884 Protein #

## ALIGNMENTS

RESULT 1  
AAB48318  
ID AAB48318 standard; protein; 312 AA.  
XX  
AC AAB48318;  
XX  
DT 11-SEP-2003 (revised)  
DT 20-APR-2001 (first entry)  
XX  
DE T. pallidum ssp. endemicum (Bosnia) acidic repeat protein (arp).  
XX  
KW Treponema pallidum; acidic repeat protein; arp; immunogenic; syphilis;  
XX yaws; bejel.  
XX  
OS Treponema pallidum; ssp. endemicum.  
XX  
PN WO200077466-A2.  
XX  
PD 21-DEC-2000.  
XX  
PF 14-JUN-2000; 2000WO-US016425.  
XX  
PR 14-JUN-1999; 99US-0138981P.  
XX  
PX (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
XX  
PY Liu H, Steiner B, Rhodes B;  
XX WPI; 2001-080711/09.  
XX N-PSDB; AAC84645.  
XX  
PT Detection of Treponema pallidum in blood, saliva, etc., by detecting  
PT formation of a complex between immunogenic peptides of acidic repeat  
PT protein of the bacterium and an antibody present in the biological  
PT sample.  
XX  
PS Claim 15; Fig 10; 73pp; English.  
XX  
CC The invention relates to a method of detecting presence of Treponema  
CC pallidum (TP), anti-treponemal antibodies (Ab) or both in a biological  
CC sample that involves contacting an acidic repeat protein (arp), or one or  
CC more isolated immunogenic TP peptides of arp with an Ab containing  
CC biological sample and then detecting the formation of a complex between  
CC immunogenic peptides and Ab. The presence of the complex indicates the  
CC presence of TP. The method is thus useful for diagnosing syphilis, yaws,  
CC and bejel diseases. The immunogenic peptides or the Abs raised against  
CC arp, as part of an immunogenic composition, are useful for inducing a  
CC protective immune response against syphilis, yaws or bejel caused by TP.





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OM protein - protein search, using sw model

Run on: April 28, 2005, 16:36:51 ; Search time 81.2695 Seconds  
(without alignments)  
2192.749 Million cell updates/sec

Title: US-10-017-168-22

Perfect score: 1776  
Sequence: 1 MFVRSDMPFKNTAVETISNLE.....AVLENFORFGKAFLLKKAR 348

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: UniProt 03.\*

1: uniprot\_sprot.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1776	100.0	348	09ALV7	Q9ALV7 treponema p
2	1743.5	98.2	393	093CA3	Q93CA3 treponema p
3	1726	97.2	428	09ALV6	Q9ALV6 treponema p
4	1656	93.2	548	093CA4	Q93CA4 treponema p
5	1043.5	58.8	432	051953	051953 treponema p
6	1042	58.7	227	083449	083449 treponema p
7	963	54.2	256	083448	083448 treponema p
8	472	26.6	458	073NG7	073NG7 treponema d
9	164.5	9.3	410	096214	096214 encephalito
10	163.5	9.1	1112	063G96	063G96 bacillus ce
11	152.5	8.6	466	06NE60	06NE60 encephalito
12	152.5	8.6	614	094674	094674 magnetospir
13	152	8.6	675	0871R0	0871R0 plasmidium
14	152	8.6	675	0871R0	0871R0 neurospora
15	151.5	8.5	519	07S118	07S118 neurospora
16	149.5	8.4	394	0964D0	0964D0 encephalito
17	149.5	8.4	453	1 PTP1 ENCH	076273 streptococc
18	146.5	8.2	1167	07SH54	07SH54 neurospora
19	145.5	8.2	1070	081YT0	081YT0 bacillus an
20	144	8.1	687	07S7J3	07S7J3 neurospora
21	141.5	8.0	915	06FM18	06FM18 candida gla
22	140	7.9	601	0711B3	0711B3 streptococc
23	135.5	7.6	3277	07NN14	07NN14 gloebacter
24	135.5	7.6	796	096579	096579 trypanosoma
25	135.5	7.6	891	06NVT0	06NVT0 xenopus tro
26	135.5	7.6	1964	059947	059947 streptococc
27	135	7.6	443	076153	076153 periplaneta
28	135	7.6	1963	08DPR5	08DPR5 streptococc
29	134.5	7.5	834	091R12	091R12 raphanus sa
30	133.5	7.5	834	071S18	071S18 homo sapien
31	133.5	7.5	979	0879Y2	0879Y2 plasmidium

32	133.5	7.5	10578	2	Q81SF5	Q81SF5 caenorhabdi
33	133.5	7.5	18519	2	Q81SF6	Q81SF6 caenorhabdi
34	133.5	7.5	18534	2	Q81SF7	Q81SF7 caenorhabdi
35	133	7.5	722	2	Q26893	Q26893 trypanosoma
36	133	7.5	779	2	Q7YRG3	Q7YRG3 canis fami
37	133	7.5	2032	2	Q7SD73	Q7SD73 neurospora
38	133	7.5	2768	2	Q9VC00	Q9VC00 drosophila
39	132.5	7.5	812	2	Q9AT64	Q9AT64 oryza sativ
40	132	7.4	486	2	Q96RX3	Q96RX3 homo sapien
41	132	7.4	1554	2	Q7RXX1	Q7RXX1 plasmidium
42	131.5	7.4	407	1	IE68_SHV21	Q01042 salmellitine
43	131.5	7.4	2004	2	Q97GP7	Q97GP7 streptococc
44	131	7.4	459	1	CAH9_HUMAN	Q16790 homo sapien
45	131	7.4	486	2	Q86VQ3	Q86VQ3 homo sapien

## ALIGNMENTS

## RESULT 1

09ALV7 PRELIMINARY; PRT; 348 AA.

AC 09ALV7; 01-JUN-2001 (TREMBLrel. 17, Created)  
DT 01-DEC-2001 (TREMBLrel. 19, last sequence update)  
DT 01-OCT-2002 (TREMBLrel. 22, last annotation update)  
DE Acidic repeat protein.  
GN Name=arp; Treponema pallidum (subsp. pertenue) (Yaws treponeme).  
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.  
OX NCBI\_TaxID=168;  
RN 1;  
RP SEQUENCE FROM N.A.  
RC STRAIN=CDC2;  
RA Liu H., Steiner B.;  
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AB342806; AAK01460.2; -; E4A446BD82344592 CRC64;  
SQ SEQUENCE 348 AA; 37936 MW; E4A446BD82344592 CRC64;

Query Match 100.0%; Score 1776; DB 2; Length 348;  
Best Local Similarity 100.0%; Pred. No. 7.9e-100; Indels 0; Gaps 0;  
Matches 348; Conservative 0; Mismatches 0;

QY	1	MFVRSDMPFKNTAVETISNLEKNKAQAVVIGHAGIPGLLVSLAPAAAGLGIVQAVAV	60
DB	1	MFVRSDMPFKNTAVETISNLEKNKAQAVVIGHAGIPGLLVSLAPAAAGLGIVQAVAV	60
QY	61	RVRTCTGVGGSGTODGLSLSLSRVPAQNDPLSSPPAGHTVPEYRTVTFDDRR	120
DB	61	RVRTCTGVGGSGTODGLSLSLSRVPAQNDPLSSPPAGHTVPEYRTVTFDDRR	120
QY	121	LVSPLSRVEDVPKVPSPASERGEREVEDVPKVPSPASERGEREVEDVPKVPSPAS	180
DB	121	LVSPLSRVEDVPKVPSPASERGEREVEDVPKVPSPASERGEREVEDVPKVPSPAS	180
QY	181	EREGEREVEDVPKVPSPASERGEREVEDVPKVPSPASERGEREVEDVPKVPSPAS	240
DB	181	EREGEREVEDVPKVPSPASERGEREVEDVPKVPSPASERGEREVEDVPKVPSPAS	240
QY	241	PLSSESEIVPEQKGRAPVITPEGARGIQPGYVQIVAFHAIQVOSIVHRYGVEY	300
DB	241	PLSSESEIVPEQKGRAPVITPEGARGIQPGYVQIVAFHAIQVOSIVHRYGVEY	300
QY	301	PLAVEODIHGKVRFTVCVGVQVQDERGAVLENFORFGKAFLLKKAR	348
DB	301	PLAVEODIHGKVRFTVCVGVQVQDERGAVLENFORFGKAFLLKKAR	348

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OM protein - protein search, using sw model

Run on: April 28, 2005, 17:24:23 ; Search time 104.3 Seconds  
(without alignments)  
77.871 Million cell updates/sec

Title: US-10-017-168-10

Sequence: 1 PKNTAVEISNLEKNAQAQAVV 21

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 500 summaries

Database : A\_Geneseq\_16Dec04:\*

- 1: geneeqp19808:\*
- 2: geneeqp19908:\*
- 3: geneeqp20008:\*
- 4: geneeqp20018:\*
- 5: geneeqp20028:\*
- 6: geneeqp20038:\*
- 7: geneeqp20038:\*
- 8: geneeqp20048:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	100	100.0	21	4	AA048322 T. pallid
2	100	100.0	232	4	AA048317 T. pallid
3	100	100.0	312	4	AA048318 T. pallid
4	100	100.0	432	4	AA048316 T. pallid
5	48	48.0	924	5	AB054116 Lactococc
6	48	48.0	924	5	AB054116 Lactococc
7	47	47.0	559	6	AB050839 S. pneumo
8	47	47.0	559	6	AB050839 S. pneumo
9	47	47.0	559	6	AB050839 S. pneumo
10	47	47.0	559	6	AB050839 S. pneumo
11	47	47.0	559	6	AB050839 S. pneumo
12	46	46.0	719	5	AB050839 S. pneumo
13	45	45.0	127	5	AB050839 S. pneumo
14	45	45.0	127	5	AB050839 S. pneumo
15	45	45.0	127	5	AB050839 S. pneumo
16	45	45.0	127	5	AB050839 S. pneumo
17	45	45.0	127	5	AB050839 S. pneumo
18	45	45.0	127	5	AB050839 S. pneumo
19	45	45.0	127	5	AB050839 S. pneumo
20	45	45.0	127	5	AB050839 S. pneumo
21	45	45.0	127	5	AB050839 S. pneumo
22	45	45.0	127	5	AB050839 S. pneumo
23	45	45.0	127	5	AB050839 S. pneumo
24	45	45.0	127	5	AB050839 S. pneumo
25	45	45.0	127	5	AB050839 S. pneumo

25	44	44.0	100	5	AB040001 Human ORF
26	44	44.0	126	4	AA050260 C. glutami
27	44	44.0	223	4	AA052129 P. putill
28	44	44.0	223	4	AA052129 P. putill
29	44	44.0	223	4	AA052129 P. putill
30	44	44.0	223	4	AA052129 P. putill
31	44	44.0	223	4	AA052129 P. putill
32	44	44.0	223	4	AA052129 P. putill
33	44	44.0	223	4	AA052129 P. putill
34	44	44.0	223	4	AA052129 P. putill
35	44	44.0	223	4	AA052129 P. putill
36	44	44.0	223	4	AA052129 P. putill
37	44	44.0	223	4	AA052129 P. putill
38	44	44.0	223	4	AA052129 P. putill
39	44	44.0	223	4	AA052129 P. putill
40	44	44.0	223	4	AA052129 P. putill
41	44	44.0	223	4	AA052129 P. putill
42	44	44.0	223	4	AA052129 P. putill
43	44	44.0	223	4	AA052129 P. putill
44	44	44.0	223	4	AA052129 P. putill
45	44	44.0	223	4	AA052129 P. putill
46	44	44.0	223	4	AA052129 P. putill
47	44	44.0	223	4	AA052129 P. putill
48	44	44.0	223	4	AA052129 P. putill
49	44	44.0	223	4	AA052129 P. putill
50	44	44.0	223	4	AA052129 P. putill
51	44	44.0	223	4	AA052129 P. putill
52	44	44.0	223	4	AA052129 P. putill
53	44	44.0	223	4	AA052129 P. putill
54	44	44.0	223	4	AA052129 P. putill
55	44	44.0	223	4	AA052129 P. putill
56	44	44.0	223	4	AA052129 P. putill
57	44	44.0	223	4	AA052129 P. putill
58	44	44.0	223	4	AA052129 P. putill
59	44	44.0	223	4	AA052129 P. putill
60	44	44.0	223	4	AA052129 P. putill
61	44	44.0	223	4	AA052129 P. putill
62	44	44.0	223	4	AA052129 P. putill
63	44	44.0	223	4	AA052129 P. putill
64	44	44.0	223	4	AA052129 P. putill
65	44	44.0	223	4	AA052129 P. putill
66	44	44.0	223	4	AA052129 P. putill
67	44	44.0	223	4	AA052129 P. putill
68	44	44.0	223	4	AA052129 P. putill
69	44	44.0	223	4	AA052129 P. putill
70	44	44.0	223	4	AA052129 P. putill
71	44	44.0	223	4	AA052129 P. putill
72	44	44.0	223	4	AA052129 P. putill
73	44	44.0	223	4	AA052129 P. putill
74	44	44.0	223	4	AA052129 P. putill
75	44	44.0	223	4	AA052129 P. putill
76	44	44.0	223	4	AA052129 P. putill
77	44	44.0	223	4	AA052129 P. putill
78	44	44.0	223	4	AA052129 P. putill
79	44	44.0	223	4	AA052129 P. putill
80	44	44.0	223	4	AA052129 P. putill
81	44	44.0	223	4	AA052129 P. putill
82	44	44.0	223	4	AA052129 P. putill
83	44	44.0	223	4	AA052129 P. putill
84	44	44.0	223	4	AA052129 P. putill
85	44	44.0	223	4	AA052129 P. putill
86	44	44.0	223	4	AA052129 P. putill
87	44	44.0	223	4	AA052129 P. putill
88	44	44.0	223	4	AA052129 P. putill
89	44	44.0	223	4	AA052129 P. putill
90	44	44.0	223	4	AA052129 P. putill
91	44	44.0	223	4	AA052129 P. putill
92	44	44.0	223	4	AA052129 P. putill
93	44	44.0	223	4	AA052129 P. putill
94	44	44.0	223	4	AA052129 P. putill
95	44	44.0	223	4	AA052129 P. putill
96	44	44.0	223	4	AA052129 P. putill
97	44	44.0	223	4	AA052129 P. putill
98	44	44.0	223	4	AA052129 P. putill

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# OM protein - protein search, using sw model

Run on: April 28, 2005, 17:40:43 ; Search time 19.95 Seconds  
(without alignments)  
101.281 Million cell updates/sec

Title: US-10-017-168-10

Perfect score: 100  
Sequence: 1 PKNTAVEISNLEKNKAQAVV 21

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 500 summaries

Database :  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	100.0	256	2	F71326	hypothetical prote
2	48.0	924	2	C66725	chromosome segrega
3	47.0	559	2	D95055	PTS system, lactos
4	47.0	559	2	A97925	probable phosphor
5	46.0	719	2	A81358	hypothetical prote
6	45.0	265	2	T35512	hypothetical prote
7	44.5	404	2	F84999	hypothetical prote
8	44.0	244	1	G8BPP4	head size determin
9	44.0	244	2	P42465	head size determin
10	44.0	778	2	T17679	proline-rich prote
11	44.0	1136	2	F96564	hypothetical prote
12	43.0	554	2	F86244	hypothetical prote
13	43.0	961	2	T49228	plasma membrane H+
14	42.0	115	2	H75491	conserved hypotet
15	42.0	265	2	AC2084	ABC transporter, A
16	42.0	309	2	A42921	transcription elon
17	42.0	369	2	T29207	aspartokinase (AKH
18	42.0	446	2	D90238	macronuclear alpha
19	42.0	476	2	D71200	internalin protein
20	42.0	495	2	A41221	protein-tyrosine-p
21	42.0	673	2	AT1143	phlyl protein homo
22	42.0	795	2	T20939	hypothetical prote
23	42.0	1187	1	A53661	hypothetical prote
24	41.0	1217	2	H82707	hypothetical prote
25	41.0	143	2	G90873	unknown protein en
26	41.0	164	2	D85745	hypothetical prote
27	41.0	228	2	A13082	Flidz protein (Ad27
28	41.0	228	2	G98203	membrane-bound tet
29	41.0	237	1	S56137	

30	41	41.0	241	2	B97019
31	41	41.0	301	2	AF1257
32	41	41.0	301	2	AB1620
33	41	41.0	326	1	T21924
34	41	41.0	331	1	A30929
35	41	41.0	331	2	F85811
36	41	41.0	331	2	AC0752
37	41	41.0	331	2	P90963
38	41	41.0	331	2	H64957
39	41	41.0	331	2	T27866
40	41	41.0	555	2	F96914
41	41	41.0	619	2	C64696
42	41	41.0	797	2	AH1302
43	41	41.0	797	2	AH1674
44	41	41.0	803	1	E70041
45	41	41.0	1070	2	T30848
46	41	41.0	1188	1	A57064
47	41	41.0	1216	2	S60613
48	41	41.0	1250	2	A39578
49	41	41.0	2152	2	T45583
50	40.5	40.5	244	2	T22779
51	40.5	40.5	244	2	A75184
52	40	40.0	92	2	A11101
53	40	40.0	92	2	A11463
54	40	40.0	149	2	S53383
55	40	40.0	189	2	C64496
56	40	40.0	239	2	T02551
57	40	40.0	314	2	D70313
58	40	40.0	315	2	A96597
59	40	40.0	345	2	T41355
60	40	40.0	404	2	G85088
61	40	40.0	405	2	H71984
62	40	40.0	451	2	G82218
63	40	40.0	506	2	F86253
64	40	40.0	555	2	C95911
65	40	40.0	584	2	B82936
66	40	40.0	595	2	B97866
67	40	40.0	606	1	OXB05M
68	40	40.0	616	2	C71648
69	40	40.0	631	2	A64578
70	40	40.0	760	2	H84427
71	40	40.0	765	1	JT0383
72	40	40.0	767	2	T19690
73	40	40.0	808	2	T51138
74	40	40.0	876	2	AB1177
75	40	40.0	876	2	AF1534
76	40	40.0	1062	2	F83335
77	40	40.0	1062	2	T30830
78	40	40.0	1287	2	AF2031
79	40	40.0	1375	2	T13822
80	40	40.0	1526	2	T13823
81	39.5	39.5	156	2	D81343
82	39.5	39.5	345	2	E71843
83	39	39.0	49	2	T13184
84	39	39.0	68	2	B44993
85	39	39.0	117	2	T29913
86	39	39.0	128	2	C84873
87	39	39.0	128	2	B72230
88	39	39.0	180	2	T33142
89	39	39.0	212	2	C75093
90	39	39.0	243	2	C95313
91	39	39.0	243	2	F95288
92	39	39.0	253	2	G97267
93	39	39.0	259	2	A98098
94	39	39.0	259	2	E85943
95	39	39.0	259	2	H65071
96	39	39.0	292	2	AB2893
97	39	39.0	292	2	E97668
98	39	39.0	294	2	F87397
99	39	39.0	297	2	S17474
100	39	39.0	311	2	E82915
101	39	39.0	313	2	AD1285
102	39	39.0	314	2	H71802

1-acyl-sn-glycerol  
GTP binding protei  
GTP binding protei  
hypothetical prote  
flagellar motor sw  
hypothetical prote  
flagellar motor sw  
flagellar motor sw  
flagellar motor sw  
hypothetical prote  
membrane-associate  
hypothetical prote  
primosomal replica  
probable copper-tr  
buffy receptor - p  
protein-tyrosine-p  
SSD1 protein - yea  
hypothetical prote  
hypothetical prote  
ATP-binding transp  
3. subtilis YabO p  
probable membrane  
hypothetical prote  
probable carboxyme  
riboflavin kinase  
hypothetical prote  
Surl homolog - fis  
hypothetical prote  
probable carboxyme  
sensor histidine X  
hypothetical prote  
probable protein,  
conserved hypotet  
DNA primase (EC 2.  
NADH2 dehydrogenas  
DNA primase (EC 2.  
conserved hypotet  
anthranilate synth  
hypothetical prote  
probable glutamate  
cation transportin  
RND multidrug effl  
hypothetical prote  
two-component hybr  
frazzled gene prot  
frazzled gene prot  
oxygen-independent  
hypothetical prote  
flagellar repetiti  
hypothetical prote  
hypothetical prote  
hypothetical prote  
cytochrome-c oxida  
probable GntR-type  
PBP superfamily hy  
hypothetical prote  
hypothetical prote  
metal dependant be  
hypothetical prote  
dihydrodipicolinat  
hypothetical prote  
ribosomal protein  
glycerate dehydrog  
probable outer mem



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OM protein - protein search, using sw model

Run on: April 28, 2005, 17:24:23 ; Search time 94.3667 Seconds  
(without alignments)  
77.871 Million cell updates/sec

Title: US-10-017-168-7  
Perfect score: 92  
Sequence: 1 LVSPUREVEDAPKVEPAPAS 19

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues  
Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 500 summaries

Database : A\_Genesep216Dec04:\*  
1: Genesep219908:\*  
2: Genesep219908:\*  
3: Genesep220018:\*  
4: Genesep220018:\*  
5: Genesep220028:\*  
6: Genesep220038:\*  
7: Genesep220038:\*  
8: Genesep220048:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	92	100.0	19 4 AAB48319	Aab48319 T. pallid
2	81.5	88.6	432 4 AAB48316	Aab48316 T. pallid
3	77.5	84.2	232 4 AAB48317	Aab48317 T. pallid
4	77.5	84.2	312 4 AAB48318	Aab48318 T. pallid
5	69	75.0	20 4 AAB48320	Aab48320 T. pallid
6	64	69.6	20 4 AAB48329	Aab48329 T. pallid
7	60	65.2	20 4 AAB48327	Aab48327 T. pallid
8	55	59.8	20 4 AAB48328	Aab48328 T. pallid
9	53	57.6	20 4 AAB48330	Aab48330 T. pallid
10	47	51.1	299 4 AAB48312	Aab48312 E. coli c
11	47	51.1	299 6 ABU28671	Abu28671 Protein e
12	45	48.9	131 8 ADU65364	Adg65364 Novel hum
13	45	48.9	197 4 AAM80072	Aam80072 Human pro
14	45	48.9	198 4 AAM79088	Aam79088 Human pro
15	45	48.9	198 6 ABR57259	Abt57259 Human cys
16	45	48.9	198 8 ABM82286	Abm82286 Tumour-as
17	44	47.8	612 4 ABB71474	Abb71474 Drosophi
18	44	47.8	763 2 AAY24094	Aay24094 Mouse BPC
19	43	46.7	403 4 ADS44816	AdS44816 Bacterial
20	43	46.7	434 3 AAG38717	Aag38717 Bacterial
21	43	46.7	434 3 AAG608216	Aag608216 Arabidops
22	43	46.7	434 5 ABB92639	Abb92639 Herpicida
23	43	46.7	792 4 AAG82199	Aag82199 S. epider
24	43	46.7	801 5 ABP40739	Abp40739 Staphyloc
25	43	46.7	801 8 ADS08045	AdS08045 Staphyloc

26	42.5	46.2	137 4 AAU43202	Aau43202 Propionib
27	42.5	46.2	137 6 ABM39721	Abm39721 Propionib
28	42.5	46.2	425 4 AAU57221	Aau57221 Propionib
29	42.5	46.2	425 6 ABM53740	Abm53740 Propionib
30	42.5	46.2	481 6 ABM65884	Abm65884 Propionib
31	42	45.7	51 4 AAU51468	Aau51468 Propionib
32	42	45.7	51 6 ABM47987	Abm47987 Propionib
33	42	45.7	103 7 ABF59039	Abf59039 Human pol
34	42	45.7	160 5 ABP39059	Abp39059 Staphyloc
35	42	45.7	160 8 ADS07044	AdS07044 Staphyloc
36	42	45.7	198 8 ABBA4986	Abba4986 Listeria
37	42	45.7	254 8 ADS30522	AdS30522 Bacterial
38	42	45.7	411 7 ABO69856	AbO69856 Pseudomon
39	42	45.7	503 2 AAM27133	Aam27133 Squalene
40	42	45.7	557 8 ABG71238	Abg71238 Tumour su
41	42	45.7	783 8 ADP04469	Adp04469 Sea equir
42	42	45.7	3816 3 AAY27708	Aay27708 S. antibi
43	42	45.7	591 4 ABBA4553	Abba4553 Mouse wou
44	41.5	45.1	591 7 ADB85248	AdB85248 Rat calne
45	41.5	45.1	591 7 ADB61368	AdB61368 Rat Prote
46	41.5	45.1	591 7 ADB61376	AdB61376 Rat Prote
47	41.5	45.1	591 7 ADB61380	AdB61380 Rat Prote
48	41.5	45.1	591 7 ADB61372	AdB61372 Rat Prote
49	41.5	45.1	591 7 ADB60129	AdB60129 Rat Prote
50	41.5	45.1	816 8 ADS25042	AdS25042 Bacterial
51	41	44.6	21 4 AAB48325	Aab48325 T. pallid
52	41	44.6	21 4 AAU49135	Aau49135 Propionib
53	41	44.6	55 5 ABM45654	Abm45654 Propionib
54	41	44.6	167 3 AAB58948	AbB58948 Breaat an
55	41	44.6	240 7 ADC94548	AdC94548 E. faeciu
56	41	44.6	256 8 ABM82052	Abm82052 Tumour-as
57	41	44.6	336 7 ADE31058	AdE31058 Human dia
58	41	44.6	355 6 ABU02384	Abu02384 S. pneumo
59	41	44.6	355 6 ABP81460	Abp81460 Streptoco
60	41	44.6	355 6 ABU46232	Abu46232 Protein e
61	41	44.6	355 6 ADK46436	Adk46436 Streptoco
62	41	44.6	359 8 ADR95240	AdR95240 Novel S.
63	41	44.6	404 7 ADC00263	AdC00263 Enteroha
64	41	44.6	437 4 AAB50661	AbB50661 C. elegan
65	41	44.6	523 7 ADD48146	AdD48146 Rat Prote
66	41	44.6	572 2 AAB68486	AbB68486 Mouse ULI
67	41	44.6	572 5 ABB63228	AbB63228 Human ULI
68	41	44.6	572 6 ABP97908	Abp97908 Amino aci
69	41	44.6	572 6 ABM04810	Abm04810 Human di
70	41	44.6	572 7 ADD45026	AdD45026 Rat Prote
71	41	44.6	572 7 ADD45028	AdD45028 Human Pro
72	41	44.6	572 8 ADK70707	AdK70707 Collapsin
73	41	44.6	572 8 ADU84279	AdU84279 Malayan b
74	41	44.6	572 8 ADQ30613	AdQ30613 Pancreas
75	41	44.6	572 8 ADQ30608	AdQ30608 Pancreas
76	41	44.6	572 8 ADR99132	AdR99132 Dihydropy
77	41	44.6	662 2 AAY34751	Aay34751 C. pneumo
78	41	44.6	662 8 ABU26929	Abu26929 Protein e
79	41	44.6	676 8 ADK70694	AdK70694 Chicken C
80	41	44.6	683 4 ABB58151	Abb58151 Drosophi
81	41	44.6	710 8 ADQ65395	AdQ65395 Novel hum
82	41	44.6	721 2 AAW55409	Aaw55409 H. pylori
83	41	44.6	748 7 ABM85860	Abm85860 Mouse pro
84	41	44.6	785 2 AAM55663	Aam55663 H. pylori
85	41	44.6	886 4 ADN18363	Adn18363 Bacterial
86	41	44.6	887 4 ABM60629	Abm60629 Drosophi
87	41	44.6	893 4 ABG11144	Abg11144 Novel hum
88	41	44.6	897 2 AAW55737	Aaw55737 H. pylori
89	41	44.6	897 4 AAU36016	Aau36016 Helicobac
90	41	44.6	928 6 ABP55407	Abp55407 Human MDC
91	41	44.6	971 8 ADM57326	Adm57326 Recombina
92	41	44.6	1007 4 AAB50660	AbB50660 C. elegan
93	41	44.6	1253 8 ADS42264	AdS42264 Bacterial
94	41	44.6	1420 4 ABB63140	Abb63140 Drosophi
95	41	44.6	1692 4 AAU03390	Aau03390 Fusarium
96	41	44.6	1692 5 ABG92714	Abg92714 Fusarium
97	41	44.6	3726 4 ABB63947	Abb63947 Drosophi
98	40.5	44.0	243 4 AAM40099	Aam40099 Human pol

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M protein - protein search, using sw model

Run on: April 28, 2005, 17:25:43 ; Search time 88.9833 Seconds

(without alignments)  
109.341 Million cell updates/sec

Title: US-10-017-168-7

Effect score: 92

Sequence: 1 LVSPLEVEDAPKVEPAPAS 19

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Search: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 500 summaries

Database : Uniprot\_03:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

# SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Match	Length	DB	ID	Description
1	81.5	88.6	256	2	083448	083448 tleponema p
2	81.5	88.6	432	2	051953	051953 tleponema p
3	81.5	88.6	548	2	093CA4	093CA4 tleponema p
4	77.5	84.2	348	2	09ALV7	09ALV7 tleponema p
5	77.5	84.2	428	2	09ALV6	09ALV6 tleponema p
6	75	81.5	393	2	093CA3	093CA3 tleponema p
7	58	63.0	227	2	083449	083449 tleponema p
8	53	57.6	258	2	06N162	06N162 tleponema p
9	49	53.3	167	2	052680	052680 tleponema p
10	49	53.3	380	2	09AVT0	09AVT0 tleponema p
11	48	52.2	368	2	070784	070784 picea abies
12	47	51.1	299	1	YEGS_ECOLI	YEGS_ECOLI
13	47	51.1	299	2	083V54	083V54 escherichia
14	47	51.1	299	2	07UCB0	07UCB0 shigella fl
15	47	51.1	299	2	083K10	083K10 shigella fl
16	47	51.1	299	2	08PFZ2	08PFZ2 escherichia
17	47	51.1	299	2	08X7H7	08X7H7 escherichia
18	47	51.1	761	2	09D9U3	09D9U3 mus musculus
19	47	51.1	778	2	06PC00	06PC00 mus musculus
20	47	51.1	792	2	069XV8	069XV8 oryza sativ
21	47	51.1	1040	2	070G14	070G14 anopheles g
22	46	50.0	195	1	TATB_XANCP	TATB_XANCP
23	46	50.0	434	2	093X74	093X74 xanthomonas
24	46	50.0	434	2	075U06	075U06 brassica ra
25	46	50.0	2192	2	081BW7	081BW7 plasmodium
26	45	48.9	101	2	09ERH3	09ERH3 cavia sapien
27	45	48.9	137	2	06AHX3	06AHX3 homo sapien
28	45	48.9	142	2	08TET0	08TET0 homo sapien
29	45	48.9	194	2	09YF07	09YF07 aeropyrum p
30	45	48.9	198	1	DUC5_BOVIN	DUC5_BOVIN
31	45	48.9	198	1	DUC5_HUMAN	DUC5_HUMAN

32	45	48.9	198	1	DUC5_MOUSE	P60904 mus musculus
33	45	48.9	198	1	DUC5_RAT	P60905 rattus norv
34	45	48.9	204	2	0921J3	0921J3 mus musculus
35	45	48.9	390	2	081HV9	081HV9 bacillus ce
36	45	48.9	426	2	08MU99	08MU99 bacillus ce
37	45	48.9	497	2	08MPR7	08MPR7 typhosoma
38	45	48.9	542	2	023446	023446 caenorhabdi
39	45	48.9	612	2	096019	096019 dirosophila
40	45	48.9	612	2	09VG45	09VG45 dirosophila
41	45	48.9	662	1	GLGX_YERPE	GLGX_YERPE
42	45	48.9	662	2	0664T3	0664T3 yersinia pe
43	45	48.9	1135	2	09YHD3	09YHD3 yersinia ps
44	45	48.9	1247	2	080528	080528 xenopus lae
45	45	47.8	149	2	069XH7	069XH7 cercopithe
46	45	47.8	274	2	028716	028716 oryza sativ
47	45	47.8	302	2	06D9E8	06D9E8 archaeoglob
48	45	47.8	326	2	062F80	062F80 errinita car
49	45	47.8	326	2	063XN0	063XN0 burkholderi
50	45	47.8	326	2	092109	092109 mus musculu
51	45	47.8	763	2	07R1Q1	07R1Q1 giardia lam
52	45	47.8	763	2	092239	092239 mus musculu
53	45	47.8	809	2	0657N5	0657N5 mus musculu
54	45	47.8	813	2	08C9X6	08C9X6 oryza sativ
55	45	47.8	899	2	08KJ56	08KJ56 mus musculu
56	45	47.8	1025	2	089000	089000 rattus norv
57	45	47.3	193	1	NOIC_SYNY3	NOIC_SYNY3
58	45	47.3	651	2	061L49	061L49 synchocyst
59	45	46.7	230	1	PYRF_HAEIN	PYRF_HAEIN
60	45	46.7	403	1	ASSY_BACSU	ASSY_BACSU
61	45	46.7	404	2	0986G2	0986G2 haemophilus
62	45	46.7	434	1	MDA3_ARATH	MDA3_ARATH
63	45	46.7	434	2	081N45	081N45 mesembryant
64	45	46.7	477	2	093Y61	093Y61 marchantia
65	45	46.7	513	2	0948P8	0948P8 arabidopsis
66	45	46.7	672	2	070199	070199 arabidopsis
67	45	46.7	792	2	0986G2	0986G2 haemophilus
68	45	46.7	1091	2	08CPY0	08CPY0 bacillus su
69	45	46.7	4293	2	008852	008852 pseudomonas
70	45	46.2	682	2	008852	008852 mus musculu
71	45	46.2	785	1	METE_DESVH	METE_DESVH
72	45	45.7	114	2	0567E1	0567E1 desulfotolvi
73	45	45.7	139	1	YS87_MYCTU	YS87_MYCTU
74	45	45.7	139	1	YT11_MYCBO	YT11_MYCBO
75	45	45.7	192	2	094GC9	094GC9 mycobacteri
76	45	45.7	198	1	SCPB_LISMO	SCPB_LISMO
77	45	45.7	198	2	071Y64	071Y64 listeria mo
78	45	45.7	208	1	CP23_CHICK	CP23_CHICK
79	45	45.7	208	2	07Y5U0	07Y5U0 gallus gall
80	45	45.7	224	2	0715F2	0715F2 caenorhabdi
81	45	45.7	243	2	0806C8	0806C8 cercopithe
82	45	45.7	244	2	0821E4	0821E4 chlamydomo
83	45	45.7	244	2	08JHB7	08JHB7 gallus gall
84	45	45.7	255	2	065JF0	065JF0 gallus gall
85	45	45.7	255	2	0986C0	0986C0 bacillus li
86	45	45.7	402	2	08UCB8	08UCB8 rhizobium i
87	45	45.7	404	2	09X6W3	09X6W3 agrobacteri
88	45	45.7	404	2	092VD9	092VD9 rhizobium m
89	45	45.7	405	2	07CWP7	07CWP7 agrobacteri
90	45	45.7	417	2	09HG95	09HG95 mucor indic
91	45	45.7	460	2	09HKK1	09HKK1 thermoplas
92	45	45.7	460	2	06G0P1	06G0P1 brachydanio
93	45	45.7	482	2	0721V4	0721V4 thermus the
94	45	45.7	505	2	07V583	07V583 prochloroco
95	45	45.7	506	1	ER11_BRANA	ER11_BRANA
96	45	45.7	515	2	072J64	072J64 brassica na
97	45	45.7	582	2	06AX30	06AX30 thermus the
98	45	45.7	626	2	0902T2	0902T2 xenopus lae
99	45	45.7	636	2	09CA83	09CA83 brachydanio
100	45	45.7	663	2	09WA03	09WA03 arabidopsis
101	45	45.7	669	2	089BR3	089BR3 arabidopsis
102	45	45.7	768	2	08SRC6	08SRC6 bradyrhizob
103	45	45.7	873	2	08RTT3	08RTT3 encephalito
104	45	45.7	873	2	06SF00	06SF00 uncultured

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OM protein - protein search, using sw model

Run on: April 28, 2005, 17:40:43 ; Search time 18.05 Seconds

(without alignment)  
101.281 Million cell updates/sec

Title: US-10-017-168-7

Perfect score: 92

Sequence: 1 LVSPUREVEDAPKVEEPAS 19

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database:

PIR\_79: \*  
1: pirl: \*  
2: pirl2: \*  
3: pirl3: \*  
4: pirl4: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	81.5	88.6	256	2	F71326
2	58	63.0	227	2	G71326
3	49	53.3	167	2	SS2220
4	47	51.1	299	2	F85835
5	47	51.1	299	2	D90990
6	47	51.1	299	2	E64975
7	45	48.9	194	2	F72775
8	45	48.9	198	2	S70515
9	45	48.9	198	2	I52655
10	45	48.9	342	2	T29707
11	45	48.9	662	2	AG0479
12	45	48.9	1135	2	T30561
13	44	47.8	274	2	C69444
14	44	47.8	624	2	T27096
15	43.5	47.3	193	2	FEYB01
16	43	46.7	230	2	BE4111
17	43	46.7	403	2	B69589
18	43	46.7	434	2	T47545
19	42	45.7	139	2	B70925
20	42	45.7	198	2	AF1318
21	42	45.7	209	2	A36344
22	42	45.7	402	2	A52894
23	42	45.7	404	2	H95937
24	42	45.7	405	2	T44600
25	42	45.7	405	2	H97669
26	42	45.7	506	2	T07942
27	42	45.7	646	2	E96828
28	41.5	45.1	137	2	B71136
29	41.5	45.1	566	1	NIPSRP

30	41.5	45.1	591	2	B54354	calnexin precursor
31	41.5	45.1	591	2	C54354	calnexin precursor
32	41	44.6	210	2	S41631	hypoxanthine phosph
33	41	44.6	217	2	G75219	hypothetical prote
34	41	44.6	224	2	F69601	hypothetical prote
35	41	44.6	243	2	E81652	cytidylate kinase
36	41	44.6	355	2	S11152	conserved hypothet
37	41	44.6	355	2	F98084	oligopeptide trans
38	41	44.6	355	2	F95220	hypothetical prote
39	41	44.6	404	2	G90781	hypothetical prote
40	41	44.6	428	2	D85642	hypothetical prote
41	41	44.6	404	2	T32952	hypothetical prote
42	41	44.6	498	2	PC6300	hypothetical prote
43	41	44.6	510	2	G72464	synaptoemargin X -
44	41	44.6	572	2	S58889	hypothetical prote
45	41	44.6	572	2	JC5317	collapsin response
46	41	44.6	572	2	S49985	dihydropyrimidinas
47	41	44.6	648	2	T20144	hypothetical prote
48	41	44.6	662	2	B72114	hypothetical prote
49	41	44.6	662	2	E86509	RNA ligase Cp0624
50	41	44.6	866	2	H69378	DNA ligase (import
51	41	44.6	897	2	F71816	conserved hypothet
52	41	44.6	971	2	D70128	DNA polymerase I -
53	41	44.6	1151	2	T24541	conserved hypothet
54	41	44.6	2717	2	A34203	hypothetical prote
55	41	44.6	3759	2	A35085	DNA-binding protei
56	41	44.6	3828	2	T13857	lithothorax protei
57	40.5	44.0	439	2	T16414	hypothetical prote
58	40.5	44.0	1330	2	H89567	protein T08A9.1 (i
59	40.5	44.0	2186	2	H89960	hypothetical prote
60	40	43.5	181	2	T24194	hypothetical prote
61	40	43.5	217	2	B71203	hypothetical prote
62	40	43.5	265	2	G69319	conserved hypothet
63	40	43.5	306	2	F70603	hypothetical prote
64	40	43.5	325	2	S58146	hypothetical prote
65	40	43.5	357	2	A33950	YOPM protein - Yer
66	40	43.5	399	2	JC4215	T-cell reactive pr
67	40	43.5	409	2	T43599	yop targeted effec
68	40	43.5	438	2	D70528	hypothetical prote
69	40	43.5	467	2	AH3437	DNA repair protei
70	40	43.5	624	2	PC6003	surface membrane p
71	40	43.5	732	1	S73715	cytadherence acces
72	40	43.5	743	2	G83726	assimilatory nitra
73	40	43.5	747	1	TNBR82	82.3K alpha trans
74	40	43.5	1146	2	S07915	RF2 protein - Yeas
75	40	43.5	1146	2	A48206	calcium-activated
76	40	43.5	1405	2	T27969	hypothetical prote
77	39.5	42.9	203	2	A12385	peroxiredoxin (imp
78	39.5	42.9	356	2	A46164	calnexin - human
79	39.5	42.9	589	2	D89997	acetylactate synth
80	39.5	42.9	592	2	A46673	calnexin precursor
81	39.5	42.9	592	2	I53260	calnexin - human
82	39.5	42.9	593	1	A37273	calnexin precursor
83	39.5	42.9	809	2	T11695	phospholipase D (E
84	39	42.4	56	2	E83079	hypothetical prote
85	39	42.4	132	2	AH2584	hypothetical prote
86	39	42.4	132	2	G97366	hypothetical prote
87	39	42.4	231	2	H64466	nrd1 protein (limp
88	39	42.4	246	2	H72497	hypothetical prote
89	39	42.4	263	2	C70741	probable NH(3)-dep
90	39	42.4	267	2	E72538	hypothetical prote
91	39	42.4	281	1	S34626	probable HRSa prot
92	39	42.4	284	2	H87524	translation elonga
93	39	42.4	315	2	B99607	hypothetical prote
94	39	42.4	317	2	AD1542	oxidoreductases ho
95	39	42.4	317	2	AF1184	oxidoreductases ho
96	39	42.4	369	2	A39157	probable RNA helic
97	39	42.4	374	2	AE2337	hypothetical prote
98	39	42.4	393	2	JB0180	phosphopentomutase
99	39	42.4	433	2	T06407	monodehydroascorba
100	39	42.4	433	2	A55333	monodehydroascorba
101	39	42.4	434	2	JU0182	monodehydroascorba
102	39	42.4	439	2	E97079	sugar-binding peri





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OM protein - protein search, using sw model

Run on: April 28, 2005, 17:40:43 ; Search time 19 seconds  
(without alignments)  
101.281 Million cell updates/sec

Title: US-10-017-168-8  
Perfect score: 100  
Sequence: 1 SREVEDAPKVEPASEREGG 20

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 500 summaries

Database :  
1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	100	100.0	256	2	F71326		hypothetical prote
2	73	73.0	227	2	G71326		hypothetical prote
3	51	51.0	434	2	T47545		monodehydroascorba
4	48	48.0	1135	2	T30561		scythe protein - A
5	47	47.0	1151	2	T24541		hypothetical prote
6	46.5	46.5	467	2	AH3437		DNA repair protein
7	46	46.0	178	2	E95994		hypothetical prote
8	45	45.0	198	2	S70515		hypothetical prote
9	46	46.0	198	2	S70515		hypothetical prote
10	46	46.0	437	2	C87688		cysteine string pr
11	46	46.0	1408	2	T47671		PolC bifunctional
12	45	45.0	382	2	T08301		P-glycoprotein-lik
13	45	45.0	434	2	TJ0182		monodehydroascorba
14	44.5	44.5	297	2	F86839		phosphate ABC tran
15	44.5	44.5	1189	2	T51481		hypothetical prote
16	44	44.0	220	2	A75287		response regulator
17	44	44.0	297	2	F70572		hypothetical prote
18	44	44.0	624	2	T27096		hypothetical prote
19	44	44.0	1106	2	TVHUGL		transforming prote
20	43.5	43.5	304	2	T10212		hypothetical prote
21	43	43.0	99	2	A55819		nonhistone chromos
22	43	43.0	133	2	D70910		hypothetical prote
23	43	43.0	179	2	F71854		probable outer mem
24	43	43.0	220	2	E64660		peptidoglycan asso
25	43	43.0	308	2	T17946		CAMP response elem
26	43	43.0	312	2	E64072		hypothetical prote
27	43	43.0	344	2	JC5602		spermidine/putresc
28	43	43.0	344	2	JC5602		CAMP response elem
29	43	43.0	344	2	JC5601		CAMP response elem

30	43	43.0	428	2	T32952	hypothetical prote
31	43	43.0	547	2	E70650	phosphoglucosylase
32	43	43.0	873	2	T16282	hypothetical prote
33	42.5	42.5	153	1	B69215	conserved hypothet
34	42.5	42.5	249	2	JH0629	cleavage signal-1
35	42	42.0	217	2	C37944	CAMP response elem
36	42	42.0	229	2	B37944	CAMP response elem
37	42	42.0	229	2	A37944	CAMP response elem
38	42	42.0	238	2	S36101	CAMP response elem
39	42	42.0	341	2	S20827	CAMP response elem
40	42	42.0	723	1	S26686	CAMP response elem
41	42	42.0	852	2	RRWQTN	RNA-directed RNA p
42	42	42.0	1076	2	T06310	C27D11.1 protein -
43	42	42.0	137	2	B72720	hypothetical prote
44	41	41.0	139	2	B70925	hypothetical prote
45	41	41.0	152	2	A87261	hypothetical prote
46	41	41.0	159	2	T10699	hypothetical prote
47	41	41.0	210	2	C87305	hypothetical prote
48	41	41.0	254	1	G69884	conserved hypothet
49	41	41.0	355	2	S11152	oligopeptide trans
50	41	41.0	355	2	F98084	hypothetical prote
51	41	41.0	355	2	F95820	hypothetical prote
52	41	41.0	416	1	A42879	advanced glycosyla
53	41	41.0	435	2	T05019	hypothetical prote
54	41	41.0	437	2	T06407	monodehydroascorba
55	41	41.0	437	2	C35147	integrase homolog
56	41	41.0	437	2	D70528	hypothetical prote
57	41	41.0	438	2	PC6300	synaptochrome X -
58	41	41.0	498	2	E84250	acetyl-CoA synthet
59	41	41.0	542	2	I53106	gene glt protein -
60	41	41.0	564	2	G72412	hypothetical prote
61	41	41.0	623	2	T46020	hypothetical prote
62	41	41.0	632	2	T44834	hypothetical prote
63	41	41.0	712	2	T02565	disease resistance
64	41	41.0	771	2	T33022	hypothetical prote
65	41	41.0	798	2	B66322	36A14.8 protein -
66	41	41.0	874	2	AC3477	DNA mismatch repair
67	41	41.0	915	2	C64513	hypothetical prote
68	41	41.0	1272	2	H89960	hypothetical prote
69	41	41.0	2186	2	T42629	tenascin-X - bovin
70	41	41.0	4135	2	H72556	hypothetical prote
71	40.5	40.5	101	2	B71618	mezoletic surface
72	40.5	40.5	272	2	ED58MC	immediate-early pn
73	40.5	40.5	595	1	H83184	phosphoenolpyruvat
74	40.5	40.5	878	2	S23003	trax protein - Esc
75	40	40.0	198	2	AP1318	hypothetical prote
76	40	40.0	249	2	B96022	probable dehydroge
77	40	40.0	276	2	T44319	hypothetical prote
78	40	40.0	278	1	TPHUTW	tropomn T, slow B
79	40	40.0	291	2	D64043	citrate (pro-3S)-1
80	40	40.0	306	2	G89988	hypothetical prote
81	40	40.0	306	2	T32583	hypothetical prote
82	40	40.0	327	2	S54287	hypothetical prote
83	40	40.0	335	2	G82596	otin protein - vib
84	40	40.0	339	2	S21265	phage-related prot
85	40	40.0	346	2	H82993	acetylserotonin O-
86	40	40.0	357	2	H71122	conserved hypothet
87	40	40.0	357	2	T30730	hypothetical prote
88	40	40.0	383	2	C83202	hypothetical prote
89	40	40.0	389	2	A25281	alginate biosynthe
90	40	40.0	394	2	T23981	apolipoprotein A-I
91	40	40.0	421	2	S27490	hypothetical prote
92	40	40.0	449	2	T22946	catalase (EC 1.11.
93	40	40.0	461	2	H84567	hypothetical prote
94	40	40.0	475	2	C72505	probable diacylgly
95	40	40.0	512	2	S35551	transcription fact
96	40	40.0	524	2	JH0395	DNA-binding protei
97	40	40.0	583	2	UC7657	mannan endo-1,4-be
98	40	40.0	591	2	T47395	hypothetical prote
99	40	40.0	615	2	T21449	hypothetical prote
100	40	40.0	620	2	H69626	PTS fructose-speci
101	40	40.0	635	2		
102	40	40.0				

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# OM protein - protein search, using sw model

Run on: April 28, 2005, 17:25:43 ; Search time 93.6667 Seconds  
(without alignments)  
109.341 Million cell updates/sec

Title: US-10-017-168-8

Perfect score: 100

Sequence: 1 SREVEDAPKVEPASEREGG 20

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: UniProt\_03.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	100	100.0	256	083448	083448 treponema p
2	100	100.0	432	051953	051953 treponema p
3	100	100.0	548	093C44	093C44 treponema p
4	96	96.0	348	09ALV7	09ALV7 treponema p
5	96	96.0	428	09ALV6	09ALV6 treponema p
6	92	92.0	393	093CA3	093CA3 treponema p
7	73	73.0	227	083449	083449 treponema p
8	54	54.0	434	093X74	093X74 brasiica ra
9	54	54.0	434	075U06	075U06 brasiica ol
10	52	52.0	2192	081BW7	081BW7 plasmodium
11	51	51.0	434	1 MDA3	MDA3 arabisops
12	49	49.0	983	06A974	06A974 propionibac
13	48	48.0	265	065U70	065U70 bacillus li
14	48	48.0	572	1 STR_CHRYO	STR_CHRYO chromobacte
15	48	48.0	769	075BK7	075BK7 ashbya goss
16	48	48.0	1135	2 O9IMX8	O9IMX8 xenopus lae
17	48	48.0	1159	2 O9IMX8	O9IMX8 cericophilhec
18	47	47.0	612	2 O9VGA5	O9VGA5 drosophila
19	47	47.0	612	2 O9VGA5	O9VGA5 drosophila
20	47	47.0	1165	2 O7UKP6	O7UKP6 caenorhabdi
21	47	47.0	1475	2 O6C8P1	O6C8P1 yarrowia li
22	46.5	46.5	294	2 O6UGG2	O6UGG2 enterobacte
23	46.5	46.5	467	2 O8YFN4	O8YFN4 bruceella me
24	46.5	46.5	467	2 O8G279	O8G279 bruceella su
25	46	46.0	137	2 O6AHX3	O6AHX3 homo sapien
26	46	46.0	142	2 O8ETU0	O8ETU0 homo sapien
27	46	46.0	178	2 O92UB5	O92UB5 rhizobium m
28	46	46.0	198	1 DUC5_BOVIN	DUC5_BOVIN bos taurus
29	46	46.0	198	1 DUC5_HUMAN	DUC5_HUMAN homo sapien
30	46	46.0	198	1 DUC5_MOUSE	DUC5_MOUSE mus musculu
31	46	46.0	198	1 DUC5_RAT	DUC5_RAT rattus norv

32	46	46.0	204	2 O921J3	O921J3 mus musculu
33	46	46.0	228	2 O6ERP9	O6ERP9 oryza sativ
34	46	46.0	261	2 O9QUP7	O9QUP7 mus musculu
35	46	46.0	262	2 O75Z26	O75Z26 sus scrofa
36	46	46.0	262	2 O88346	O88346 mus musculu
37	46	46.0	322	2 O9D595	O9D595 mus musculu
38	46	46.0	435	2 O9XFE3	O9XFE3 oryza sativ
39	46	46.0	435	2 O652L6	O652L6 oryza sativ
40	46	46.0	437	2 O9A2L6	O9A2L6 caulobacter
41	46	46.0	649	1 DXS1_KITGR	DXS1_KITGR kitasacospo
42	46	46.0	944	2 O8CGI1	O8CGI1 mus musculu
43	46	46.0	1408	2 O9M3B9	O9M3B9 arabidopsis
44	46	46.0	156	2 O8C457	O8C457 mus musculu
45	45	45.0	131	2 O84851	O84851 oryza sativ
46	45	45.0	256	2 O8WV22	O8WV22 homo sapien
47	45	45.0	382	2 O51988	O51988 halobacteri
48	45	45.0	434	1 MDA5_CUCSA	MDA5_CUCSA cucumis sat
49	45	45.0	436	2 O8K0S3	O8K0S3 mus musculu
50	45	45.0	477	2 O93YGI	O93YGI mesembryant
51	45	45.0	579	2 O8QZS3	O8QZS3 mus musculu
52	45	45.0	582	2 O82FE9	O82FE9 streptomyce
53	45	45.0	781	2 O9SNG8	O9SNG8 oryza sativ
54	45	45.0	850	2 O7KU82	O7KU82 drosophila
55	45	45.0	943	2 P31638	P31638 drosophila
56	45	45.0	944	2 O9V862	O9V862 drosophila
57	45	45.0	1072	2 O98LC1	O98LC1 rhizobium 1
58	45	45.0	1247	2 O805Z8	O805Z8 cercopithec
59	44.5	44.5	267	1 SSF2_HUMAN	SSF2_HUMAN homo sapien
60	44.5	44.5	297	2 O9CEW6	O9CEW6 lactococcus
61	44.5	44.5	357	2 O8PPY8	O8PPY8 xanthomonas
62	44.5	44.5	584	2 O8N7H2	O8N7H2 homo sapien
63	44.5	44.5	792	2 O8CEY0	O8CEY0 staphylococ
64	44.5	44.5	964	2 O8N263	O8N263 homo sapien
65	44.5	44.5	1106	2 O8N1L3	O8N1L3 homo sapien
66	44.5	44.5	1106	2 O68DA6	O68DA6 homo sapien
67	44.5	44.5	1180	2 O8VYW7	O8VYW7 arabidopsis
68	44.5	44.5	1189	2 O9LF07	O9LF07 arabidopsis
69	44.5	44.5	1256	2 O8NEN5	O8NEN5 homo sapien
70	44.5	44.5	1259	2 O7Z7L2	O7Z7L2 homo sapien
71	44.5	44.5	1325	2 O96FW1	O96FW1 homo sapien
72	44	44.0	130	2 O9K4G3	O9K4G3 streptomyce
73	44	44.0	184	2 O8XYS0	O8XYS0 raietonia s
74	44	44.0	220	2 O9RS02	O9RS02 delnoccocus
75	44	44.0	263	2 O8MKH6	O8MKH6 bos taurus
76	44	44.0	285	2 O7PZJ6	O7PZJ6 anopheles g
77	44	44.0	297	2 O06189	O06189 mycobacteri
78	44	44.0	297	2 O7TY75	O7TY75 mycobacteri
79	44	44.0	338	2 O8ORS6	O8ORS6 triturus ca
80	44	44.0	362	2 O6AKI3	O6AKI3 brachydanio
81	44	44.0	368	2 O70784	O70784 oat sterile
82	44	44.0	450	2 O70P84	O70P84 mellitangan
83	44	44.0	483	2 O9UGT4	O9UGT4 northern ce
84	44	44.0	528	1 PGGA_HUMAN	PGGA_HUMAN homo sapien
85	44	44.0	557	2 O9NAH5	O9NAH5 caenorhabdi
86	44	44.0	579	2 O76UQ2	O76UQ2 rattus norv
87	44	44.0	609	2 O9W2U4	O9W2U4 drosophila
88	44	44.0	702	2 O9V852	O9V852 drosophila
89	44	44.0	737	2 O6YSW9	O6YSW9 oryza sativ
90	44	44.0	805	2 O8PSI4	O8PSI4 methanocarc
91	44	44.0	840	2 O7EYJ8	O7EYJ8 oryza sativ
92	44	44.0	939	2 O7ZYP9	O7ZYP9 bacillus ce
93	44	44.0	1081	2 O7SBY5	O7SBY5 neustopora
94	44	44.0	1106	1 GLI1_HUMAN	GLI1_HUMAN homo sapien
95	44	44.0	2406	2 O9BZS0	O9BZS0 homo sapien
96	44	44.0	2414	2 O9HCL7	O9HCL7 homo sapien
97	44	44.0	2414	2 O6N585	O6N585 rhodospendo
98	43.5	43.5	304	2 O9SV59	O9SV59 arabidopsis
99	43.5	43.5	499	2 O04376	O04376 arabidopsis
100	43.5	43.5	752	2 O801W4	O801W4 brachydanio
101	43	43.0	68	2 O8K8H1	O8K8H1 heliobacte
102	43	43.0	68	2 O6PY62	O6PY62 heliobacte
103	43	43.0	68	2 O6PY63	O6PY63 heliobacte
104	43	43.0	68	2 O6PY64	O6PY64 heliobacte